REMARKS

Examiner Interview

Applicants thank the Examiner, Dr. Jae W. Lee, for granting the personal interview on March 26, 2009 with Dr. John Sinclair, one of the co-inventors, and Mr. David Brook, Applicants' Attorney. At the interview, Dr. Sinclair explained the invention and the differences between the claimed invention and the prior art, particularly the Padilla *et al.* reference employing the figures attached to this Amendment. Additionally, Mr. Brook and Dr. Lee discussed the rejections under 35 U.S.C. § 112. Applicants agree with the Interview Summary prepared by Dr. Lee, a copy of which is attached. Lastly, Applicants are particularly appreciative of Dr. Lee's helpful and constructive suggestions.

Claim Listing

In the Office Action, the Examiner indicated that Claims 1, 5 and 7-25 are pending. This disposition of claims appears to be in error. Applicants respectfully point out that Claims 1, 5-27 and 29-33 are pending and Claims 26, 27 and 29-33 are withdrawn from consideration.

Amendments to the Claims

Claims 1, 5-27 and 29-33 are pending.

Claims 1, 5, 7, 8, 11-15 and 18 are amended.

Claim 1 has been amended to more particularly and distinctly point out the claimed invention. Support for Claim 1 can be found throughout the Specification, for example at page 2, line 19 through page 3, line 18.

Claims 1, 5 and 8 have been amended to recite "at least three rotational symmetry axes," instead of "a set of rotational symmetry axes extending in three dimensions" to better clarify the claimed invention.

Claims 1, 5, 7, 8, 11-15 and 18 have been amended to recite "second monomer," instead of "further monomer," to better clarify the claimed invention.

Entry of these amendments is respectfully requested.

Objection of Claim 1

Claim 1 was objected to for the recitation of "protein protomers which each comprise." Claim 1 has been amended to recite "protein protomers, wherein each protein protomer comprises" as the Examiner suggested.

Rejection of Claims 1, 5 and 7-25 Under 35 U.S.C. § 112, Second Paragraph

Claims 1, 5 and 7-25 were rejected under 35 U.S.C. § 112, second paragraph, for being indefinite. Claim 1 has been amended to clarify the claim language, namely to delete "a set of rotational symmetry axes extending in three dimension" and to recite "at least three rotational symmetry axes." Claim 1 has been amended to add a phrase "when said protomers self-assemble into the lattice" to particularly point out the claimed invention. The amendments to Claim 1 render moot the rejection against Claim 1 and all claims dependent on Claim 1.

Rejection of Claims 1, 5 and 7-25 Under 35 U.S.C. § 112, First Paragraph

Claims 1, 5 and 7-25 were rejected under 35 U.S.C. § 112, first paragraph, for lacking written description. The Examiner states that: "The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time application was filed, had possession of the claimed invention.

Applicants respectfully traverse the rejection. The written description requirement is satisfied where the specification describes the claimed invention in detail so that one skilled in the art can reasonably conclude that the inventor had possession of the claimed invention. *Vas-Cath, Inc. v. Mahurkar*, 19 U.S.P.Q.2d 1111 (Fed. Cir. 1991). Further, with respect to the genus and species, the court in *Regents of the University of California v. Eli Lilly and Co.*, 43 U.S.P.Q.2d 1398 (Fed. Cir. 1997) stated as follows:

> A description of a genus of cDNAs may be achieved by means of a recitation of a representative number of cDNAs, defined by nucleotide sequence, falling within the scope of the genus or of a recitation of structural features common to the members of the genus, which features constitute a substantial portion of the genus.(*Id.* at 1406).

Applicants are entitled to the genus claim directed to a protein lattice having a regular structure comprising a repeating unit of protein protomer(s) because Applicants had possession of the genus as evidenced by the present Specification. The Specification provides sufficient guidance for the structural and functional features common to the members of the genus and exemplifies a representative number of the genus.

In addition to the remarks made in the previous Amendment filed on July 21, 2008, Applicants point out that the Specification exemplifies a sufficient number of species and adequate amount of teachings to satisfy the written description requirement. Figure 1 of the Specification depicts an example of a protein lattice established from assembly of a protomer represented by p_4d_4. The first oligomer assembly, as exemplified in Figure 1, is human ferritin heavy chain (HFH) which belongs to an octahedral P_4 point group of order 4. The second oligomer assembly, as exemplified in Figure 1, is *E. coli* PurE which belongs to a dihedral D_4 point group of order 4.

The Specification also provides, in Figure 2, another protein lattice made from two mixed types of protomers. The first promoter of the protein lattice of Figure 2 comprises a first monomer of a first homologous oligomer assembly, namely *E. coli* dps, which belongs to a tetrahedral point group. The first monomer of the first protomer in Figure 2 is then fused to a second monomer of the first protomer, which is a monomer of a second heterologous oligomer assembly, namely bacteriophage T4 gp5 which has a cyclic point group of order 3. The second class of the protomer comprises a first monomer, which is a monomer of a heterologous oligomer assembly, namely bacteriophage T4 gp27. The first monomer of the second protomer is fused to another monomer of a third oligomer assembly, namely human PTPS which belongs to a dihedral D3 point group of order 3. The Specification, therefore, provides an example of a protein lattice which can be established from a mixture of two different types of protomers.

In addition to the examples of various protein lattices discussed above, the Specification teaches the structural and functional features common to the genus by providing the specific rotational symmetry alignment requirements for the quaternary structures of oligomer assemblies implemented in the fusion protein ("protomer") which would confer the self-assembling function of the protomor(s) into a protein lattice as discussed in the remarks of the Amendment previously filed on July, 21, 2008 (also *see*, the Specification at page 4, line 8 through page 8, line 3; page

10, line 4 through page 16, line 28; and Tables 1 and 2). The instant application provides specific teachings regarding the common structural features of the claimed invention along with their functions. Applicants' specification clearly evidences that Applicants had possession of the genus claims.

Rejection of Claims 1, 5 and 7-25 Under 35 U.S.C. § 112, First Paragraph

Claims 1, 5 and 7-25 were also rejected under 35 U.S.C. § 112, first paragraph, for lacking enablement. The Examiner states that: "...the specification, while being enabling for a protein lattice comprising a fusion protein comprising the human ferritin heavy chain (HFH) and the E. coli PurE... does not reasonably provide enablement for any protein lattice having a regular structure with a repeating unit repeating in three dimensions, the repeating unit comprising any protein protomers...The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention commensurate in scope with these claims" (Office Action, bridging paragraph between pages 13 and 14).

This rejection is in error for the following reasons. The claims as amended are enabled by the detailed teachings of the Specification and the knowledge in the art at the time the invention was made. The Examiner's focus on certainty with respect to the protomers which form a claimed protein lattice is misplaced, and does not support the rejection. Enablement does not require "certainty" for a use. Enablement requires that a person of ordinary skill in the art be able to make and use the invention without engaging in "undue experimentation" using the teachings of the specification and the knowledge in the art. The test of enablement is not whether any experiment is required, but whether, if experimentation is necessary, it is undue. *In re Angstadt*, 537 F.2d 498, 504, 190 USPQ 214, 219 (CCPA 1976).

The factors to be considered when determining enablement include: (a) the breadth of the claims; (b) the nature of the invention; (c) the state of the prior art; (d) the level of one of ordinary skill; (e) the level of predictability in the art; (f) the amount of direction provided by the inventor; (g) the existence of working examples; and (h) the quantity of experimentation needed to make or use the invention based on the content of the disclosure. *In re Wand,* 858. F2d 731, 737; 8 USPQ2d 1400, 1404 (Fed. Cir. 1988),

The Breadth and Nature of the Claims

The claimed invention is directed to the genus of protein lattices having a regular structure with a repeating unit(s) of protein protomers. Each protein protomer comprises at least two monomers fused together and the monomers each being a monomer of an oligomer assembly. The first monomer is a monomer (a subunit of a oligomer protein complex) of an oligomer assembly (an oligomer protein complex referred in the present application as "first oligomer assembly"). The first oligomer assembly has at least three rotational symmetry axes. The first monomer is fused to a second monomer which is a monomer of another oligomer assembly ("second oligomer assembly" as amended). The second oligomer assembly, according to the invention, has a rotational symmetry axis of the same order as one of the set of rotational symmetry axes of the first oligomer assembly and the rotational symmetry axis of the second oligomer assembly is aligned with the one of the rotational symmetry axes of the first oligomer assembly when the protomers self-assemble into the lattice. The protein lattice of the present invention can be used, for example, as a support in X-ray crystallography (the Specification at page 24, line 7 through page 25, line 1).

The State of the Prior Art

Methodology involved in making fusion proteins (*e.g.*, chimeric proteins) and providing suitable conditions for protomer assembly were routine at the time the invention was made. For example, the formation and production of the protomers are described in the Specification (the Specification at page 8, line 4 through page 10, line 3; at page 19, line 2 through page 21, lines 5-8). The formation and production of fusion proteins are also well known in the art (*e.g.*, WO 2000/68248, the entire teachings of which are incorporated by reference in the present application). One of ordinary skill in the art routinely created various types of fusion proteins by either recombinant technology or crosslinking technology at the time the invention was made. Suitable conditions for the protomer assembly processes for potential protomers were also well known and described in the art as taught in WO 2000/68248 (see the present Specification at page 21, lines 13-14).

The Level of One of Ordinary Skill in the Art

The level of one of ordinary skill in the art was the level of ordinary skill in structural biology and bioinformatics who are specialized in protein designs in an academic or industrial setting.

The Amount of Direction Provided By the Inventors

As stated above, an absolute certainty is not required for enablement. The requisite conditions for monomers and oligomer assembly in order for resultant protomers to form the claimed protein lattice are well described in the Specification. Specifically, the requisite rotational symmetries and alignment of oligomer assemblies of the claimed invention is well described in the Specification. The protein lattices of the present invention can be designed by selecting oligomer assemblies having appropriate symmetries (the Specification at page 4, lines 8-19). The principle by which symmetries of the lattices derive from the symmetry axes of the oligomers assemblies is also taught in detail in the Specification (the Specification at page 4, line 26 through page 8, line 3). Numerous examples of the combinations of symmetries of the oligomer assemblies which allow formation of the claimed protein lattices are also provided, for example, as enumerated in Tables 1 and 2 (the Specification at page 10, line 4 though page 16 line 28). Table 1 provides examples of homologous protomers capable of forming a protein lattice and Table 2 lists examples of heterologous protomers capable of forming a protein lattice. The Specification also teaches that information regarding possible oligomer assemblies and their rotational symmetry axes are generally available and well known in the art (the Specification at page 4, lines 13-19). Table 3 provides examples of oligomer assemblies which share a common point group as mentioned in Tables 1 and 2. Candidate monomers of the present invention, whose oligomer assemblies have the requisite symmetries and orders can be selected by referring to, for example, Tables 1, 2 and 3 of the Specification as well as information available in the art. According to the present invention, it is, therefore, the characteristics involving rotational symmetry axes of oligomer assembly and their orders that need to be identified, not the specific physical and chemical properties of a potential oligomer assembly or articulated fusion techniques. Accordingly, the present application provides sufficient guidance to make and use the present invention which is not limited to particular oligomer assemblies, but extends to oligomer assemblies having a quaternary structure with the requisite rotational symmetry and order.

The Level of Predictability in the Art

Achieving the claimed invention, once one of ordinary skill in the art understand the primary principles involved in creating the claimed protein lattice as taught in great detail in the Specification, was predictable. Previously, Applicants submitted post-filing evidence of enablement, Exhibit A, which was filed at the European Patent Office on August 16, 2006 in connection with European Patent Application No. 03753741.2. The document provides an additional 3D regular protein lattice experimentally demonstrated in accordance with the present invention in addition to the protein lattices provided in Figures 1 and 2 of the Specification. This post-filing success demonstrates the claimed invention is highly enabling and can be achieved with a high level of predictability once one of ordinary skill in the art recognizes the underlying principles of the present invention.

The Existence of Working Examples

Figure 1 of the Specification depicts an example of a protein lattice established from assembly of homogeneous protomers represented by p_4d_4. The first oligomer assembly, as exemplified in Figure 1, is human ferritin heavy chain (HFH) which belongs to an octahedral point group of order 4 (p_4). The second oligomer assembly is *E. coli* PurE which belongs to a dihedral point group of order 4 (d_4). Figure 1 of the Specification, therefore, provides an example of a protein lattice which are established from homogenous protomers, whose oligomer assemblies have a point group of order 4 and are aligned with the one of the rotational symmetry axes of the first oligomer assembly when the protomers self-assemble into the lattice.

In Figure 2, the Specification provides a more complex protein lattice formed from two mixed types of heterogeneous protomers, each represented by p_3c_{3A} and d_3c_{3A}, respectively. The first promoter of the protein lattice of Figure 2 comprises a first monomer of a first oligomer assembly, namely *E. coli* dps, which belongs to a tetrahedral point group of order 3. The first monomer of the first protomer in Figure 2 is then fused to a second monomer, which is a monomer of a second heterologous oligomer assembly, namely bacteriophage T4 gp5 having a cyclic point group of order 3. The second class of the protomer of Figure 2 comprises a first monomer which is the other monomer of the heterologous oligomer assembly of bacteriophage T4, namely T4 gp27 which belongs to a cyclic point group of order 3. The first monomer of the second protomer is, then, fused to another monomer of a third oligomer assembly, namely

human PTPS which belongs to a dihedral D_3 point group of order 3. Figure 2 of the Specification provides an example of a protein lattice which are established from a mixture of two hetergeneous protomers, whose oligomer assemblies have a point group of order 3 and are aligned with the one of the rotational symmetry axes of the first oligomer assembly when the protomers self-assemble into the lattice.

In addition, as discussed above, Applicants submitted a post-filing evidence of enablement, Exhibit A, a copy of a document filed at the European Patent Office on August 16, 2006 in connection with European Patent Application No. 03753741.2. The document describes an additional experimentally demonstrated 3D regular protein lattice in accordance with the present invention. A first oligomer assembly is a small heat shock protein (SHS) having p_4 symmetry (octahedral or cubic symmetry) and the second oligomer assembly is the streptavidin/streptag assembly having d_2 symmetry (dihedral symmetry of order 2).

The Quantity of Experimentation Needed to Make or Use the Invention Based on the Content of the Disclosure

It would only take routine experimentation, not undue experimentation, for one of ordinary skill in the art to make and use the claimed invention using the disclosure of Applicants' specification. Ample guidance on the principle involved in making and using the invention is provided and the working examples are presented in detail in the Specification as discussed above. Further, Tables 1-3 provide various types of protomers having specific rotational symmetries with specific orders suitable for forming a stable structure of the protein lattices of the claimed invention. Since the level of ordinary skill in the art was such that it would be routine experimentation to make and use the claimed protein lattices once the requisite elements for protomers suitable for forming claimed protein lattices are recognized as taught by the Specification, one of ordinary skill in the art would not have to engage in undue experimentation to make and use the claimed invention.

Further, the Examiner states that:

> It is noted by the Examiner that Exhibit A only discloses an additional example of a protein lattices, i.e., crysalins, comprising a small heat shock protein and streptavidin/streptag assembly having specific symmetry, which was obtained after filing of the instant application. However, this information does not enable

> one of skill in the art to make and use the scope of the invention as claimed because one would be left with testing all possible combinations of all protein protomers/fused monomers, optionally having any set of rotation symmetry axes, and determining which of these combination can be fused together or used together to form a protein lattice (Office Action at page 17, second paragraph).

Applicants disagree with the Examiner. Applicants are not required to teach in detail all experimental procedures for every possible protein protomer encompassed by the present claims. The ways in which appropriate oligomer assemblies are selected and methods for fusing two monomers of the chosen oligomer assemblies are well described in the Specification (see the Specification at page 8, line 25 through page 10, lines 3; page 19, lines 18-27) and was also known in the art at the time of the invention (see WO 2002/68248). Further, as discussed above, the Specification provides ample guidance on the principles for establishing the claimed protein lattices from protomers which enable the formation of such protein lattices. Therefore, given the level of one of ordinary skill in the art and predictability and it would not take undue experimentation for one of ordinary skill in the art to make and use the claimed invention based on the teachings of the Specification and what was known in the art.

In summary, the specification provides ample guidance to one of ordinary skill in the art to make and use the present invention without engaging undue experimentation. Therefore, pending Claims 1, 5 and 7-25 meet the enablement requirement under 35 U.S.C. § 112, first paragraph.

Rejection of Claims 1, 5 and 7-25 under 35 U.S.C. § 102(b)

Claims 1, 5 and 7-25 have been rejected under 35 U.S.C. § 102(b) as being anticipated by Padilla *et al.* (*The Proceedings of National Academy of Science* (PNAS), 2001, 98: 2217-2221, hereinafter, "Padilla") in view of the evidentiary reference Hestenes (retrievable from the Internet at <http://modelingnts.la.asu.edu/pdf/crystalsymmetry.pdf>).

Padilla teaches fusion proteins designed to self-assemble into an ordered structure (*i.e.*, protein layers, cages, shells or filaments). Padilla particularly teaches that protein cages, shells, layers and filaments are formed from fusion proteins consisting of two monomers ("oligomerization domains") fused with each other by a carefully chosen linker with a particular angle. Padilla teaches that "a fusion protein carries two virtual symmetry axes, one from each

oligomerization domain."[1] In Table 1, Padilla further provides a construction rule to achieve a given symmetry of oligomerization domain.[2] Padilla teaches about the importance of having a rigid linker by stating that: "If the oligomerization domains are instead fused in arbitrary or flexible ways, the fusion proteins might assemble in a irregular fashion to give a material whose structure and properties cannot be anticipated."[3] Thus, the construction of fusion proteins to generate higher order structures requires that the subunit ("oligomerization domain") be fused by a rigid connection. Padilla suggests use of an alpha helix at the terminus of each molecule. This feature is required to ensure that the respective single symmetry axis is fixed at a defined angle with respect to one another. Padilla tabulates angles that would result in either closed system (*e.g.*, a cage) or repeating system (*e.g.*, a 2-D layer).

In contrast, the present invention is directed to protein lattices having a regular structure with a repeating unit(s) of protein protomers that is not dependent on a rigid linker or the relative orientation of the monomers within the protomer. The present invention is designed to provide crystalline species having a repeating unit(s) extending in three dimensional space. Each protein protomer is chosen from higher symmetry species with symmetry axes lying along more than one coordinate axis. Specifically, each protein protomer comprises at least two monomers fused together and the monomers each being a monomer of an oligomer assembly. The first monomer is a monomer (a subunit of a oligomer protein complex) of an oligomer assembly ("first oligomer assembly"). The first oligomer assembly has at least three ("a set of") rotational symmetry axes. In a protomer, the first monomer is fused to a second monomer which is a monomer of another oligomer assembly ("second oligomer assembly"). The second oligomer assembly has at least one rotational symmetry axis of the same order as one of the at least three rotational symmetry axes of the first oligomer assembly and the rotational symmetry axis of the second oligomer is aligned with the one of the rotational symmetry axes of the first oligomer assembly when the protomers self-assemble into a protein lattice.

First, the present invention relates to a protein lattice established from protomers whose geometric rules of construction is based on the rotational symmetry axes of the "oligomer assemblies," not on those of "monomers." In contrast, the geometric rules of construction taught

---

[1] Padilla at page 2217, left column, last paragraph.
[2] *Id.*, at page 2217, right column, first paragraph.
[3] *Id.*

by Padilla are based on the fixed geometric relationship between the two symmetry axes of the two oligomerization domains ("monomers" as used in the present invention) within a fusion protein ("protomer" as used in the present invention) created by a precisely engineered linker between the two oligomerization domains ("monomers" of the protomer as used in the present invention) (see Padilla, Fig. 1b). Padilla specifically states that "a fusion protein carries two virtual symmetry axes, one from each oligomerization domain (Fig. 1*b*)"[4] (emphasis added). Applicants note that the oligomerization domains described in Padilla are equivalent to "monomers" as used in the present application.[5] Padilla also states that: "To satisfy the construction rule for a particular design, the two oligomerization domains in a fusion protein must be held together in a relative rigid fashion."[6] Because the present invention relates to a protein lattice established from protomers whose geometric rules of construction is based on the rotational symmetry axes of the "oligomer assemblies," instead of the fixed geometric relationship between the symmetry axes of the monomers generated by the rigid linkers, the present invention provides the benefit that one is not restricted by the selection of the relative orientation of the monomers within the protomer via a rigid linker.

Second, the differences between the rules of construction for the present invention and the self-assembling proteins in Padilla give rise to a significant structural differences. In the present invention, the symmetries in the regular structure are achieved by having one of the rotational symmetry axes of the second oligomer assembly aligned with the one of the rotational symmetry axes of the first oligomer assembly. In Padilla, the rotational symmetry axes of the oligomers ("oligomer assemblies") are either parallel or at an angle to each other as listed in Table 1. In Padilla, the only experimentally demonstrated structures are a filament and a cage which is a closed system. To create a closed system of cage or shell, Padilla modifies the angle of the linker (*i.e.*, the alpha helical protein), for example, 35.3° for the structure shown in Fig. 1(e) and 54.7° for the structure shown in Fig. 2(c). When the linker is designed to create an angle to establish a closed system, the oligomerization domains lose their parallel alignment with each other. Therefore, in contrast to the present invention, the geometry of the symmetry

---

[4] Padilla at page 2217, left column, last paragraph.
[5] "Following specific geometric rules, two oligomerization domains are connected by genetic manipulation into a single larger molecule called a fusion protein." Padilla at page 2217, left column, third paragraph.
[6] Padilla at page 2217, right column, second paragraph.

elements of Padilla's system (e.g., a cage or shell) becomes intersecting (see Padilla Fig. 1*b*). Accordingly, Padilla's closed system does not anticipate the present invention.

Even if the alpha helix linker of Padilla is in an orientation so that the rotational symmetry axes of the two oligomers are parallel with each other, Padilla's fusion protein only results in a two-dimensional crystalline layer (*see* Padilla, Fig. 1(d)). Even in this case, the rotational symmetry axes of the two oligomers are not aligned, but are merely parallel.

For an open structure extending in three directions, Padilla's teaching is limited to a theoretical rule of construction that is not demonstrated experimentally. Even in this theoretical rule of construction, the teachings are limited to the use of a linker to provide specific angles between the rotational symmetry axes of a dimeric oligomerization domain and a trimeric oligomerization domain that are set out in Table 1 under the heading "Three-dimensional crystals."[7] As result, none of the structures demonstrated by Padilla resembles the protein lattice/matrix extending in three dimensions demonstrated in the present application (see the Specification, Figs. 1 and 2).

Third, the first oligomer assembly of the present invention has at least three rotational symmetries. In contrast, Padilla only demonstrates the fusion of proteins with a single symmetry axis (see Padilla Fig. 1*b*). The teachings of Padilla are restricted to dimers and trimers having a single axis of symmetry. Although the oligomers are shown in Fig. 1a as semi-circles and triangles which appear in the schematic drawing to be symmetrical about a line perpendicular to the rotational symmetry axis of order 2 or 3, this is not in fact the case because the monomers are folded proteins. Thus, the dimers and trimers have a single rotational symmetry axis of order 2 and 3 respectively as shown in Fig. 1a. Padilla does not teach that the use of oligomers having at least three rotational symmetries in the "structure" ("first or second oligomer assembly" as used in the present application). Specifically, Padilla does not teach that trimeric bromoperoxidase complex or dimeric M1 influenza virus matrix protein complex has at least three rotational symmetry axes, these being respectively a trimer and a dimer having a single rotational symmetry axis.

Fourth, in the present invention, the symmetries in the regular structure are achieved by having the same order N of the rotational symmetry axis in both the first and second oligomer

---

[7] Padilla at page 2218, right column, Table 1.

assemblies. In the present invention, the fusion of monomers is made along this common symmetry axis. This is an important distinction from the teachings by Padilla (see the present Specification at page 6, lines 13-29). Padilla's teachings are silent on this aspect of construction because Padilla uses monomers (the dimers and trimers) whose respective single rotational symmetry axes are not aligned with each other. Instead, Padilla's oligomerization domains are fixed by a rigid linker to carefully facilitate the desired angle (see Padilla Fig. 1*b*) and Padilla's construction does not involve the N-fold fusion described in the present invention.

Fifth, self-assembling proteins by Padilla always require a precisely engineered linker which connects the two oligomerization domains in order to create an angle of symmetry axes between the two oligomerization domains. In contrast, the present invention does not require a linker (see the Specification at page 8, lines 28-31) as long as the monomers are fused with each other in a manner that the resulting oligomer assemblies have the rotational symmetry suitable for self-assembly as taught in the Specification. Fusion of the monomers, for example, can occur along a pre-existing symmetry axis common to both assemblies (N-fold fusion). Hence, no engineering of the fusion for a specific angle facilitated by the carefully designed linker is required in the present invention.

In sum, for the foregoing reasons, the arrangement of the repeating unit, and hence the resultant lattice as a whole in the present invention is dependent on the symmetries of the oligomer assembly, not on the relative orientation of the monomers within an individual protomer as required in Padilla. Due to these fundamental differences in construction, the claimed protein lattice is clearly not anticipated by the self-assembling proteins of Padilla.

CONCLUSION

In view of the above amendments and remarks, it is believed that all claims are in condition for allowance, and it is respectfully requested that the application be passed to issue. If the Examiner feels that a telephone conference would expedite prosecution of this case, the Examiner is invited to call the undersigned.

Respectfully submitted,

HAMILTON, BROOK, SMITH & REYNOLDS, P.C.

By David E. Brook

David E. Brook
Registration No.: 22,592
Telephone: (978) 341-0036
Facsimile: (978) 341-0136

Concord, MA 01742-9133
Date: 6/5/09